

# Exhibit C

## Blast of SEQ ID NO: 1 versus human genome

MEGABLAST 1.2.3-Paracel [2001-11-20]

### Reference:

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),  
"A greedy algorithm for aligning DNA sequences",  
J Comput Biol 2000; 7(1-2):203-14.  
Database: Homo\_sapiens.latestgp.masked.fa  
33,840 sequences; 200,810,911,373 total letters

Query= LEX121seqidl  
(747 letters)

Sequences producing significant alignments:

Score (bits)	E Value
-----------------	------------

AC135034.1.27032.29361  
AC025418.23.1.83000  
AC135034.1.59399.65233

287	5e-75
287	5e-75
174	5e-41

>AC135034.1.27032.29361  
Length = 2330

Score = 287 bits (145), Expect = 5e-75  
Identities = 145/145 (100%)  
Strand = Plus / Plus

Query: 451 ttacagtgttgtggccaacataattacacagactggataaagaataagaacaaagaaaaat 510  
|||||  
Sbjct: 1180 ttacagtgttgtggccaacataattacacagactggataaagaataagaacaaagaaaaat 1239

Query: 511 tcaggacaggtgccatgttcttgcacaaagtcaactttaagaaaatggttttgtgatgag 570  
|||||  
Sbjct: 1240 tcaggacaggtgccatgttcttgcacaaagtcaactttaagaaaatggttttgtgatgag 1299

Query: 571 ccaactgaatgcaacttaccttgagg 595  
|||||  
Sbjct: 1300 ccaactgaatgcaacttaccttgagg 1324

>AC025418.23.1.83000  
Length = 83000

Score = 287 bits (145), Expect = 5e-75  
Identities = 145/145 (100%)  
Strand = Plus / Minus

Query: 451 ttacagtgttgtggccaacataattacacagactggataaagaataagaacaaagaaaaat 510  
|||||  
Sbjct: 48068 ttacagtgttgtggccaacataattacacagactggataaagaataagaacaaagaaaaat 48009

Query: 511 tcaggacaggtgccatgttcttgcacaaagtcaactttaagaaatggttttgtgatgag 570  
|||||  
Sbjct: 48008 tcaggacaggtgccatgttcttgcacaaagtcaactttaagaaaatggttttgtgatgag 47949

Query: 571 ccactgaatgcaacttaccttgagg 595  
|||||  
Sbjct: 47948 ccactgaatgcaacttaccttgagg 47924

Score = 250 bits (126), Expect = 1e-63  
Identities = 126/126 (100%)  
Strand = Plus / Minus

Query: 139 gatgaaaataatcacttcacatgtacatcttctcaaatgttgattggaatgggatcttct 198  
|||||  
Sbjct: 58492 gatgaaaataatcacttcacatgtacatcttctcaaatgttgattggaatgggatcttct 58433

Query: 199 actgttctttttgtctattgggttatataggaattcacaacgaaatcagatgggtccta 258  
|||||  
Sbjct: 58432 actgttctttttgtctattgggttatataggaattcacaacgaaatcagatgggtccta 58373

Query: 259 attgtg 264  
|||||  
Sbjct: 58372 attgtg 58367

Score = 224 bits (113), Expect = 6e-56  
Identities = 113/113 (100%)  
Strand = Plus / Minus

Query: 338 aggttcagcaactatggcatgacaaaattgattttgtcatttctgagtatggatctaaag 397  
|||||  
Sbjct: 50207 aggttcagcaactatggcatgacaaaattgattttgtcatttctgagtatggatctaaag 50148

Query: 398 ataagcctgaagatataaccaagtggactattctgaatgccttacagaaaaca 450  
|||||  
Sbjct: 50147 ataagcctgaagatataaccaagtggactattctgaatgccttacagaaaaca 50095

Score = 174 bits (88), Expect = 5e-41  
Identities = 88/88 (100%)  
Strand = Plus / Minus

Query: 593 agggttgtgaaaataaaatcagtgcatgggtataatgttaatgtgttaacctaatacggaa 652  
|||||  
Sbjct: 46442 agggttgtgaaaataaaatcagtgcatgggtataatgttaatgtgttaacctaatacggaa 46383

Query: 653 ttaactttggacttttaacttcagaggt 680  
|||||

Sbjct: 46382 ttaactttg tttttaacttcagaggt 46355

Score = 155 bits (78), Expect = 5e-35  
Identities = 78/78 (100%)  
Strand = Plus / Minus

Query: 264 gtatgcagtattgataacatggacctttgctgttcaggttgactttcagcattcatcat 323  
|||||  
Sbjct: 53869 gtatgcagtattgataacatggacctttgctgttcaggttgactttcagcattcatcat 53810

Query: 324 cacaagaaagaggaggt 341  
|||||  
Sbjct: 53809 cacaagaaagaggaggt 53792

Score = 147 bits (74), Expect = 1e-32  
Identities = 74/74 (100%)  
Strand = Plus / Minus

Query: 66 gggtcttggacttttattcatgggatttgggtgcatggctcttattagatagaaataattt 125  
|||||  
Sbjct: 60260 gggtcttggacttttattcatgggatttgggtgcatggctcttattagatagaaataattt 60201

Query: 126 tttaacagcttttg 139  
|||||  
Sbjct: 60200 tttaacagcttttg 60187

Score = 141 bits (71), Expect = 7e-31  
Identities = 71/71 (100%)  
Strand = Plus / Minus

Query: 677 aggttttccaagtctcattaacagtttgtttcttcaaaaacatcaagaatataatccatg 736  
|||||  
Sbjct: 45026 aggttttccaagtctcattaacagtttgtttcttcaaaaacatcaagaatataatccatg 44967

Query: 737 cagaaatgtga 747  
|||||  
Sbjct: 44966 cagaaatgtga 44956

Score = 135 bits (68), Expect = 4e-29  
Identities = 68/68 (100%)  
Strand = Plus / Minus

Query: 1 atgttaagaaataacaaaacaataattattaagtactttcttaatctcattaatggagct 60  
|||||  
Sbjct: 60414 atgttaagaaataacaaaacaataattattaagtactttcttaatctcattaatggagct 60355

Query: 61     ttcttggt  
              |||||  
Sbjct: 60354 ttcttggt 60347

>AC135034.1.59399.65233  
Length = 5835

Score = 174 bits (88), Expect = 5e-41  
Identities = 88/88 (100%)  
Strand = Plus / Minus

Query: 593     agggttgtgaaaataaaatcagtgcatggtataatgttaatgtgttaaccttaatcgga 652  
              |||||  
Sbjct: 5352 agggttgtgaaaataaaatcagtgcatggtataatgttaatgtgttaaccttaatcgga 5293

Query: 653     ttaactttggacttttaacttcagaggt 680  
              |||||  
Sbjct: 5292 ttaactttggacttttaacttcagaggt 5265

Score = 141 bits (71), Expect = 7e-31  
Identities = 71/71 (100%)  
Strand = Plus / Minus

Query: 677     aggttttccaagtctcattaacagtttggtttcttcaaaaacatcaagaatataatccatg 736  
              |||||  
Sbjct: 3942 aggttttccaagtctcattaacagtttggtttcttcaaaaacatcaagaatataatccatg 3883

Query: 737     cagaaatgtga 747  
              |||||  
Sbjct: 3882 cagaaatgtga 3872